

# SEQUENCE LISTING

<110> Kapeller-Libermann, Rosana  
White, David  
MacBeth, Kyle J.

<120> 2786, A NOVEL HUMAN AMINOPEPTIDASE

<130> 5800-62

<140> US 09/443,795

<141> 1999-11-19

<160> 7

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 650

<212> PRT

<213> Homo sapiens

<400> 1

Met	Ala	Ser	Gly	Glu	His	Ser	Pro	Gly	Ser	Gly	Ala	Ala	Arg	Arg	Pro
1				5					10					15	
Leu	His	Ser	Ala	Gln	Ala	Val	Asp	Val	Ala	Ser	Ala	Ser	Asn	Phe	Arg
			20					25					30		
Ala	Phe	Glu	Leu	Leu	His	Leu	His	Leu	Asp	Leu	Arg	Ala	Glu	Phe	Gly
		35					40					45			
Pro	Pro	Gly	Pro	Gly	Ala	Gly	Ser	Arg	Gly	Leu	Ser	Gly	Thr	Ala	Val
	50					55					60				
Leu	Asp	Leu	Arg	Cys	Leu	Glu	Pro	Glu	Gly	Ala	Ala	Glu	Leu	Arg	Leu
65					70				75						80
Asp	Ser	His	Pro	Cys	Leu	Glu	Val	Thr	Ala	Ala	Leu	Arg	Arg	Arg	Glu
				85					90					95	
Arg	Pro	Gly	Ser	Glu	Glu	Pro	Pro	Ala	Glu	Pro	Val	Ser	Phe	Tyr	Thr
			100					105						110	
Gln	Pro	Phe	Ser	His	Tyr	Gly	Gln	Ala	Leu	Cys	Val	Ser	Phe	Pro	Gln
		115					120					125			
Pro	Cys	Arg	Ala	Ala	Glu	Arg	Leu	Gln	Val	Leu	Leu	Thr	Tyr	Arg	Val
		130				135					140				
Gly	Glu	Gly	Pro	Gly	Val	Cys	Trp	Leu	Ala	Pro	Glu	Gln	Thr	Ala	Gly
145					150				155						160
Lys	Lys	Lys	Pro	Phe	Val	Tyr	Thr	Gln	Gly	Gln	Ala	Val	Leu	Asn	Arg
				165					170					175	
Ala	Phe	Phe	Pro	Cys	Phe	Asp	Thr	Pro	Ala	Val	Lys	Tyr	Lys	Tyr	Ser
			180					185					190		
Ala	Leu	Ile	Glu	Val	Pro	Asp	Gly	Phe	Thr	Ala	Val	Met	Ser	Ala	Ser
		195					200					205			
Thr	Trp	Glu	Lys	Arg	Gly	Pro	Asn	Lys	Phe	Phe	Phe	Gln	Met	Cys	Gln
	210					215						220			
Pro	Ile	Pro	Ser	Tyr	Leu	Ile	Ala	Leu	Ala	Ile	Gly	Asp	Leu	Val	Ser
225					230					235					240
Ala	Glu	Val	Gly	Pro	Arg	Ser	Arg	Val	Trp	Ala	Glu	Pro	Cys	Leu	Ile
				245					250					255	

Asp	Ala	Ala	Asn	Glu	Glu	Tyr	Asn	Gly	Val	Ile	Glu	Glu	Phe	Leu	Ala	260	265	270
Thr	Gly	Glu	Lys	Leu	Phe	Gly	Pro	Tyr	Val	Trp	Gly	Arg	Tyr	Asp	Leu	275	280	285
Leu	Phe	Met	Pro	Pro	Ser	Phe	Pro	Phe	Gly	Gly	Met	Glu	Asn	Pro	Cys	290	295	300
Leu	Thr	Phe	Val	Thr	Pro	Cys	Leu	Leu	Ala	Gly	Asp	Arg	Ser	Leu	Ala	305	310	315
Asp	Val	Ile	Ile	His	Glu	Ile	Ser	His	Ser	Trp	Phe	Gly	Asn	Leu	Val	325	330	335
Thr	Asn	Ala	Asn	Trp	Gly	Glu	Phe	Trp	Leu	Asn	Glu	Gly	Phe	Thr	Met	340	345	350
Tyr	Ala	Gln	Arg	Arg	Ile	Ser	Thr	Ile	Leu	Phe	Gly	Ala	Ala	Tyr	Thr	355	360	365
Cys	Leu	Glu	Ala	Ala	Thr	Gly	Arg	Ala	Leu	Leu	Arg	Gln	His	Met	Asp	370	375	380
Ile	Thr	Gly	Glu	Glu	Asn	Pro	Leu	Asn	Lys	Leu	Arg	Val	Lys	Ile	Glu	385	390	395
Pro	Gly	Val	Asp	Pro	Asp	Asp	Thr	Tyr	Asn	Glu	Thr	Pro	Tyr	Glu	Lys	405	410	415
Gly	Phe	Cys	Phe	Val	Ser	Tyr	Leu	Ala	His	Leu	Val	Gly	Asp	Gln	Asp	420	425	430
Gln	Phe	Asp	Ser	Phe	Leu	Lys	Ala	Tyr	Val	His	Glu	Phe	Lys	Phe	Arg	435	440	445
Ser	Ile	Leu	Ala	Asp	Asp	Phe	Leu	Asp	Phe	Tyr	Leu	Glu	Tyr	Phe	Pro	450	455	460
Glu	Leu	Lys	Lys	Lys	Arg	Val	Asp	Ile	Ile	Pro	Gly	Phe	Glu	Phe	Asp	465	470	475
Arg	Trp	Leu	Asn	Thr	Pro	Gly	Trp	Pro	Pro	Tyr	Leu	Pro	Asp	Leu	Ser	485	490	495
Pro	Gly	Asp	Ser	Leu	Met	Lys	Pro	Ala	Glu	Glu	Leu	Ala	Gln	Leu	Trp	500	505	510
Ala	Ala	Glu	Glu	Leu	Asp	Met	Lys	Ala	Ile	Glu	Ala	Val	Ala	Ile	Ser	515	520	525
Pro	Trp	Lys	Thr	Tyr	Gln	Leu	Val	Tyr	Phe	Leu	Asp	Lys	Ile	Leu	Gln	530	535	540
Lys	Ser	Pro	Leu	Pro	Pro	Gly	Asn	Val	Lys	Lys	Leu	Gly	Asp	Thr	Tyr	545	550	555
Pro	Ser	Ile	Ser	Asn	Ala	Arg	Asn	Ala	Glu	Leu	Arg	Leu	Arg	Trp	Gly	565	570	575
Gln	Ile	Val	Leu	Lys	Asn	Asp	His	Gln	Glu	Asp	Phe	Trp	Lys	Val	Lys	580	585	590
Glu	Phe	Leu	His	Asn	Gln	Gly	Lys	Gln	Lys	Tyr	Thr	Leu	Pro	Leu	Tyr	595	600	605
His	Ala	Met	Met	Gly	Gly	Ser	Glu	Val	Ala	Gln	Thr	Leu	Ala	Lys	Glu	610	615	620
Thr	Phe	Ala	Ser	Thr	Ala	Ser	Gln	Leu	His	Ser	Asn	Val	Val	Asn	Tyr	625	630	635
Val	Gln	Gln	Ile	Val	Ala	Pro	Lys	Gly	Ser							645	650	

<210> 2

<211> 2459

<212> DNA

<213> Homo sapiens

<220>  
 <221> CDS  
 <222> (62)...(2011)

<221> misc\_feature  
 <222> (1)...(3107)  
 <223> n = A,T,C or G

```

<400> 2
gcggccgcgt cgacctcccc tcgggttcgc ggcccggccg gtgagcaacg gctctgcggc      60
c atg gcg agc ggc gag cat tcc ccc ggc agc ggc gcg gcc cgg cgg ccg      109
  Met Ala Ser Gly Glu His Ser Pro Gly Ser Gly Ala Ala Arg Arg Pro
    1             5             10             15

ctg cac tcc gcg cag gct gtg gac gtg gcc tcg gcc tcc aac ttc cgg      157
Leu His Ser Ala Gln Ala Val Asp Val Ala Ser Ala Ser Asn Phe Arg
    20             25             30

gcc ttt gag ctg ctg cac ttg cac ctg gac ctg cgg gct gag ttc ggg      205
Ala Phe Glu Leu Leu His Leu His Leu Asp Leu Arg Ala Glu Phe Gly
    35             40             45

cct cca ggg ccc ggc gca ggg agc cgg ggg ctg agc ggc acc gcg gtc      253
Pro Pro Gly Pro Gly Ala Gly Ser Arg Gly Leu Ser Gly Thr Ala Val
    50             55             60

ctg gac ctg cgc tgc ctg gag ccc gag ggc gcc gcc gag ctg cgg ctg      301
Leu Asp Leu Arg Cys Leu Glu Pro Glu Gly Ala Ala Glu Leu Arg Leu
    65             70             75             80

gac tcg cac ccg tgc ctg gag gtg acg gcg gcg gcg ctg cgg cgg gag      349
Asp Ser His Pro Cys Leu Glu Val Thr Ala Ala Ala Leu Arg Arg Glu
    85             90             95

cgg ccc ggc tcg gag gag ccg cct gcg gag ccc gtg agc ttc tac acg      397
Arg Pro Gly Ser Glu Glu Pro Pro Ala Glu Pro Val Ser Phe Tyr Thr
    100            105            110

cag ccc ttc tcg cac tat ggc cag gcc ctg tgc gtg tcc ttc ccg cag      445
Gln Pro Phe Ser His Tyr Gly Gln Ala Leu Cys Val Ser Phe Pro Gln
    115            120            125

ccc tgc cgc gcc gcc gag cgc ctc cag gtg ctg ctc acc tac cgc gtc      493
Pro Cys Arg Ala Ala Glu Arg Leu Gln Val Leu Leu Thr Tyr Arg Val
    130            135            140

ggg gag gga ccc ggg gtt tgc tgg ttg gct ccc gag cag aca gca gga      541
Gly Glu Gly Pro Gly Val Cys Trp Leu Ala Pro Glu Gln Thr Ala Gly
    145            150            155            160

aag aag aag ccc ttc gtg tac acc cag ggc cag gct gtc cta aac cgg      589
Lys Lys Lys Pro Phe Val Tyr Thr Gln Gly Gln Ala Val Leu Asn Arg
    165            170            175

gcc ttc ttc cct tgc ttc gac acg cct gct gtt aaa tac aag tat tca      637
Ala Phe Phe Pro Cys Phe Asp Thr Pro Ala Val Lys Tyr Lys Tyr Ser
    180            185            190

```

gct ctt att gag gtc cca gat ggc ttc aca gct gtg atg agt gct agc Ala Leu Ile Glu Val Pro Asp Gly Phe Thr Ala Val Met Ser Ala Ser 195 200 205	685
acc tgg gag aag aga ggt cca aat aag ttc ttc ttc cag atg tgt cag Thr Trp Glu Lys Arg Gly Pro Asn Lys Phe Phe Phe Gln Met Cys Gln 210 215 220	733
ccc atc ccc tcc tat ctg ata gct ttg gcc atc gga gat ctg gtt tcg Pro Ile Pro Ser Tyr Leu Ile Ala Leu Ala Ile Gly Asp Leu Val Ser 225 230 235 240	781
gct gaa gtt gga ccc agg agc cgg gtg tgg gct gag ccc tgc ctg att Ala Glu Val Gly Pro Arg Ser Arg Val Trp Ala Glu Pro Cys Leu Ile 245 250 255	829
gat gct gcc aat gag gag tac aac ggg gtg ata gaa gaa ttt ttg gca Asp Ala Ala Asn Glu Glu Tyr Asn Gly Val Ile Glu Glu Phe Leu Ala 260 265 270	877
aca gga gag aag ctt ttt gga cct tat gtt tgg gga agg tat gac ttg Thr Gly Glu Lys Leu Phe Gly Pro Tyr Val Trp Gly Arg Tyr Asp Leu 275 280 285	925
ctc ttc atg cca ccg tcc ttt cca ttt gga gga atg gag aac cct tgt Leu Phe Met Pro Pro Ser Phe Pro Phe Gly Gly Met Glu Asn Pro Cys 290 295 300	973
ctg acc ttt gtc acc ccc tgc ctg cta gct ggg gac cgc tcc ttg gca Leu Thr Phe Val Thr Pro Cys Leu Leu Ala Gly Asp Arg Ser Leu Ala 305 310 315 320	1021
gat gtc atc atc cat gag atc tcc cac agt tgg ttt ggg aac ctg gtc Asp Val Ile Ile His Glu Ile Ser His Ser Trp Phe Gly Asn Leu Val 325 330 335	1069
acc aac gcc aac tgg ggt gaa ttc tgg ctc aat gaa ggt ttc acc atg Thr Asn Ala Asn Trp Gly Glu Phe Trp Leu Asn Glu Gly Phe Thr Met 340 345 350	1117
tac gcc cag agg agg atc tcc acc atc ctc ttt ggc gct gcg tac acc Tyr Ala Gln Arg Arg Ile Ser Thr Ile Leu Phe Gly Ala Ala Tyr Thr 355 360 365	1165
tgc ttg gag gct gca acg ggg cgg gct ctg ctg cgt caa cac atg gac Cys Leu Glu Ala Ala Thr Gly Arg Ala Leu Leu Arg Gln His Met Asp 370 375 380	1213
atc act gga gag gaa aac cca ctc aac aag ctc cgc gtg aag att gaa Ile Thr Gly Glu Glu Asn Pro Leu Asn Lys Leu Arg Val Lys Ile Glu 385 390 395 400	1261
cca ggc gtt gac ccg gac gac acc tat aat gag acc ccc tac gag aaa Pro Gly Val Asp Pro Asp Asp Thr Tyr Asn Glu Thr Pro Tyr Glu Lys 405 410 415	1309

ggg ttc tgc ttt gtc tca tac ctg gcc cac ttg gtg ggt gat cag gat	1357
Gly Phe Cys Phe Val Ser Tyr Leu Ala His Leu Val Gly Asp Gln Asp	
420 425 430	
cag ttt gac agt ttt ctc aag gcc tat gtg cat gaa ttc aaa ttc cga	1405
Gln Phe Asp Ser Phe Leu Lys Ala Tyr Val His Glu Phe Lys Phe Arg	
435 440 445	
agc atc tta gcc gat gac ttt ctg gac ttc tac ttg gaa tat ttc cct	1453
Ser Ile Leu Ala Asp Asp Phe Leu Asp Phe Tyr Leu Glu Tyr Phe Pro	
450 455 460	
gag ctt aag aaa aag aga gtg gat atc att cca ggt ttt gag ttt gat	1501
Glu Leu Lys Lys Lys Arg Val Asp Ile Ile Pro Gly Phe Glu Phe Asp	
465 470 475 480	
cga tgg ctg aat acc ccc ggc tgg ccc ccg tac ctc cct gat ctc tcc	1549
Arg Trp Leu Asn Thr Pro Gly Trp Pro Pro Tyr Leu Pro Asp Leu Ser	
485 490 495	
cct ggg gac tca ctc atg aag cct gct gaa gag cta gcc caa ctg tgg	1597
Pro Gly Asp Ser Leu Met Lys Pro Ala Glu Glu Leu Ala Gln Leu Trp	
500 505 510	
gca gcc gag gag ctg gac atg aag gcc att gaa gcc gtg gcc atc tct	1645
Ala Ala Glu Glu Leu Asp Met Lys Ala Ile Glu Ala Val Ala Ile Ser	
515 520 525	
ccc tgg aag acc tac cag ctg gtc tac ttc ctg gat aag atc ctc cag	1693
Pro Trp Lys Thr Tyr Gln Leu Val Tyr Phe Leu Asp Lys Ile Leu Gln	
530 535 540	
aaa tcc cct ctc cct cct ggg aat gtg aaa aaa ctt gga gac aca tac	1741
Lys Ser Pro Leu Pro Pro Gly Asn Val Lys Lys Leu Gly Asp Thr Tyr	
545 550 555 560	
cca agt atc tca aat gcc cgg aat gca gag ctc cgg ctg cga tgg ggc	1789
Pro Ser Ile Ser Asn Ala Arg Asn Ala Glu Leu Arg Leu Arg Trp Gly	
565 570 575	
caa atc gtc ctt aag aac gac cac cag gaa gat ttc tgg aaa gtg aag	1837
Gln Ile Val Leu Lys Asn Asp His Gln Glu Asp Phe Trp Lys Val Lys	
580 585 590	
gag ttc ctg cat aac cag ggg aag cag aag tat aca ctt ccg ctg tac	1885
Glu Phe Leu His Asn Gln Gly Lys Gln Lys Tyr Thr Leu Pro Leu Tyr	
595 600 605	
cac gca atg atg ggt ggc agt gag gtg gcc cag acc ctc gcc aag gag	1933
His Ala Met Met Gly Gly Ser Glu Val Ala Gln Thr Leu Ala Lys Glu	
610 615 620	
act ttt gca tcc acc gcc tcc cag ctc cac agc aat gtt gtc aac tat	1981
Thr Phe Ala Ser Thr Ala Ser Gln Leu His Ser Asn Val Val Asn Tyr	
625 630 635 640	
gtc cag cag atc gtg gca ccc aag ggc agt tagaggctcg tgtgcatggc	2031

Val Gln Gln Ile Val Ala Pro Lys Gly Ser  
645 650

```

ccttgccctct tcaggctctc caggctttca gaataattgt ttgttcccaa attcctgttc 2091
cctgatcaac ttcctggagt ttatatcccc tcaggataat ctattctcta gcttaggtat 2151
ctgtgactct tgggcctctg ctctggtggg aacttacttc tctatagccc actgagcccc 2211
gagacagaga acctgcccac agctctcccc gctacaggct gcaggcactg cagggcagcg 2271
gggtattctcc tccccaccta agtctctggg aagaagtgga gaggactgat gctcttcttt 2331
tttctctttt tgtccttttt cttgctgatt ttatgcaaag ggctggcatt ctgattgttc 2391
ttttttcagg tttaatcctt attttaataa agttttcaag caaaaattaa aaaaaaaaaa 2451
aaaaaaaaa

```

<210> 3  
<211> 30  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Ribonucleoprotein Binding Site

<221> VARIANT  
<222> 27  
<223> Xaa = Any Amino Acid

```

<400> 3
Arg Lys Gly Ala Phe Ile Leu Met Asn Gln Ser Thr Val Trp Tyr Ala
 1           5           10          15
Gly Ser Cys Ile Phe Tyr Leu Ile Val Ala Xaa Phe Tyr Met
          20          25          30

```

<210> 4  
<211> 3  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Nuclear Localization Motif

<400> 4  
Lys Lys Lys  
1

<210> 5  
<211> 8  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Ribonucleoprotein Binding Motif

<400> 5  
Lys Gly Tyr Cys Phe Val Ser Tyr  
1 5

<210> 6  
<211> 5  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> potential catalytic site

<400> 6  
His Glu Ile Ser His  
1 5

<210> 7  
<211> 4  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> potential catalytic site

<400> 7  
Trp Leu Asn Glu  
1